

| GenCore version 4.5 | | | | | | | | | |
|--|-------------------------------|---|----------------------|----------------------------------|------------------|--------|---------------------------|------------|-----------------------------------|
| Copyright (c) 1993 - 2000 Compugen Ltd. | | | | | | | | | |
| OM protein - protein search, using sw model | | | | | | | | | |
| Run on: | November 20, 2000, 14:06:02 ; | Search time 9.88 Seconds | (without alignments) | 507.675 Million cell updates/sec | | | | | |
| Title: | US-09-373-230-2 | 808 | | | | | | | |
| Sequence: | 1 | INFGRLHCTTAVIIRNINDQVL.....KKDENGDKS\WMTLTLNLHQ S | 157 | | | | | | |
| Scoring table: | BLOSUM62 | | | | | | | | |
| Searched: | 87993 seqs, 31947931 residues | | | | | | | | |
| Total number of hits satisfying chosen parameters: | 87993 | | | | | | | | |
| Minimum DB seq length: | 0 | | | | | | | | |
| Maximum DB seq length: | 200000000 | | | | | | | | |
| Post-processing: | Minimum Match 0% | | | | | | | | |
| | Maximum Match 100% | | | | | | | | |
| | Maximum Match 10% | | | | | | | | |
| Database : | SwissProt_39; * | | | | | | | | |
| Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | | | | | | | | | |
| Result No. | Score | Query | Match | Length | DB | ID | Description | SUMMARIES | |
| 1 | 805 | 99.8 | 192 | 1 | IL1B_MOUSE | P70380 | mus musculus | RESULT 1 | |
| 2 | 736.5 | 91.2 | 194 | 1 | IL1B_RAT | P97635 | rattus norvegicus | IL1B MOUSE | STANDARD; |
| 3 | 538.9 | 66.6 | 193 | 1 | IL1B_HORSE | Q8X977 | equus caballus | IL1B MOUSE | ID |
| 4 | 518.5 | 64.1 | 193 | 1 | IL1B_HUMAN | Q41166 | homo sapiens | IL1B_MOUSE | AC |
| 5 | 510.9 | 63.1 | 193 | 1 | IL1B_CANFA | Q9XR01 | canis familiaris | IL1B_MOUSE | DT |
| 6 | 509.7 | 63.0 | 192 | 1 | IL1B_PIG | Q19073 | sus scrofa | IL1B_MOUSE | DT |
| 7 | 82.5 | 10.2 | 803 | 1 | IL1B_HRIMEN | P43864 | haemophilus ducreyae | IL1B_MOUSE | 30-MAY-2000 |
| 8 | 82.9 | 10.1 | 267 | 1 | IL1B_PIG | P26889 | sus scrofa | IL1B_MOUSE | (Rel. 39, Last annotation update) |
| 9 | 79.5 | 9.8 | 526 | 1 | IL1B_YEAST | P00362 | saccharomyces cerevisiae | IL1B_MOUSE | DE |
| 10 | 79.0 | 9.8 | 266 | 1 | IL1B_BOVINE | P09428 | bos taurus | IL1B_MOUSE | DE |
| 11 | 78.9 | 9.7 | 1196 | 1 | IL1B_CLOSTRIDIUM | P46801 | clostridium perfringens | IL1B_MOUSE | DE |
| 12 | 77.7 | 9.7 | 1883 | 1 | IL1A_MOUSE | P08759 | mus musculus | IL1B_MOUSE | DE |
| 13 | 76.5 | 9.5 | 167 | 1 | IL1B_METHIA | Q58219 | methanococcus fervidus | IL1B_MOUSE | DE |
| 14 | 76.5 | 9.5 | 621 | 1 | IL1B_HELPY | P56116 | helicobacte r pylori | IL1B_MOUSE | DE |
| 15 | 76.5 | 9.5 | 706 | 1 | IL1B_YEAST | P36190 | saecharomyces cerevisiae | IL1B_MOUSE | DT |
| 16 | 76.0 | 9.4 | 269 | 1 | IL1B_MACMUR | P48090 | macaca mulatta | IL1B_MOUSE | DT |
| 17 | 76.0 | 9.4 | 269 | 1 | IL1B_MACMUR | P14193 | macaca nemestrina | IL1B_MOUSE | DT |
| 18 | 75.5 | 9.3 | 270 | 1 | IL1A_MOUSE | P01582 | mus musculus | IL1B_MOUSE | DT |
| 19 | 75.5 | 9.3 | 439 | 1 | Y811_METOXA | Q88221 | methanococcus voltae | IL1B_MOUSE | DT |
| 20 | 75.5 | 9.3 | 695 | 1 | PRC_HAETIN | P45306 | haemophilus pruni | IL1B_MOUSE | DT |
| 21 | 75.0 | 9.3 | 266 | 1 | IL1B_SHEEP | P21621 | ovis aries | IL1B_MOUSE | DT |
| 22 | 75.0 | 9.3 | 268 | 1 | IL1B_MACFA | P79182 | macaca fasciata | IL1B_MOUSE | DT |
| 23 | 75.0 | 9.3 | 624 | 1 | Y811_SCPO | Q01198 | schizosaccharomyces pombe | IL1B_MOUSE | DT |
| 24 | 74.5 | 9.2 | 270 | 1 | IL1A_PIG | P88430 | sus scrofa | IL1B_MOUSE | DR |
| 25 | 74.0 | 9.2 | 269 | 1 | IL1B_HUMAN | P01584 | homo sapiens | IL1B_MOUSE | MGI; DR |
| 26 | 74.0 | 9.2 | 1139 | 1 | RBL2_HUMAN | Q88999 | homo sapiens | IL1B_MOUSE | MGI; DR |
| 27 | 73.5 | 9.1 | 589 | 1 | TRP_THEME | P08654 | thermococcus | IL1B_MOUSE | KW |
| 28 | 73.0 | 9.0 | 611 | 1 | HBS1_YEAR | P27769 | saccharomyces cerevisiae | IL1B_MOUSE | FT |
| 29 | 73.0 | 9.0 | 872 | 1 | VF2_ROTPC | P01911 | porcine rotavirus | IL1B_MOUSE | FT |
| 30 | 72.5 | 9.0 | 698 | 1 | Y806 YEAST | P88283 | saccharomyces cerevisiae | IL1B_MOUSE | SEQUENCE |
| 31 | 72.5 | 9.0 | 1010 | 1 | WNT5_DROME | P28466 | drosophila melanogaster | IL1B_MOUSE | FT |
| 32 | 72.0 | 8.9 | 207 | 1 | ATPF MYCPN | Q50327 | mycoplasma pneumoniae | IL1B_MOUSE | FT |
| 33 | 72.0 | 8.9 | 266 | 1 | IL1B_CEREL | P51745 | cervus elaphus | IL1B_MOUSE | FT |
| ALIGNMENTS | | | | | | | | | |
| Query | Match | | | | | | | 99.8% | Score 806; DB 1; Length 192; |

Best Local Similarity 99.4%; Pred. No. 7.1e-67; Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NFGRLHCTAVIRNINDQVLFVKRQPVEDMDTIDQSASEPOTRLIYMKOSEVRGL 59
 ID 36 NEGRILHCTAVIRNINDQVLFVKRQPVEDMDTIDQSASEPOTRLIYMKOSEVRGLA 60
 Db 60 AVTLSVKDSKYLTSCKNKLTISFEEMDPPEMDIDQSLFQKRVPGHNMKEFESSLYE 119
 QY 61 VTLSVKDSKYLTSCKNKLTISFEEMDPPEMDIDQSLFQKRVPGHNMKEFESSLYE 119
 ID 96 VTLSVKDSKMSLTSCKNKLTISFEEMDPPEMDIDQSLFQKRVPGHNMKEFESSLYE 155
 QY 121 GHFLACOKEDDAFKLILKKDENGDKSYMTLNUQS 157
 Db 156 GHFLACOKEDDAFKLILKKDENGDKSYMTLNUQS 192

RESULT 2
 IL18_RAT STANDARD; PRT: 194 AA.
 ID IL18_RAT P97637; 088749;
 AC 15-JUL-1998 (Rel. 36, created)
 DT 15-JUL-1998 (Rel. 36, last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE INTERLEUKIN-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR) (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).
 GN IL18 OR IGIF.
 OC Rattus norvegicus (Rat); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=SPRAGUE-DANIELY; TISSUE=ADRENAL GLAND;
 RX MEDLINE; 9712963.
 RA Conti B., Jahnq J.W., Tinti C., Son J.H., Joh T.H.; RT "Induction of interferon-gamma inducing factor in the adrenal cortex"; J. Biol. Chem. 272:2035-2037(1997).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP
 RC STRAIN=SPRAGUE-DANIELY; TISSUE=BRAIN;
 RA Culhane A.C., Hall M.D., Rothwell N.J., Luheshi G.N.; RT "Cloning of rat brain interleukin-18 cDNA"; RL Mol. Psych. 3:362-366(1998).
 CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I CELLS.
 CC --!- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>)
 CC DR EMBL; Y1131; CAA7013.1; -.

CC KW Cytokine.
 FT PROPEP 1 36 BY SIMILARITY.
 FT CHAIN 37 193 BY SIMILARITY.
 SQ SEQUENCE 193 AA; 22058 MW; 4DB1535E9004ECFAF CRC64;

Query Match Best Local Similarity 66.6%; Score 538; DB 1; Length 193; Matches 106; Conservative 23; Mismatches 23; Indels 2; Gaps 2;

QY 2 FGRLHCTAVIRNINDQVLFVKRQPVEDMDTIDQSASEPOTRLIYMKOSEVRGL 60
 ID 98 VTLSVKCEKSTLTSCKNKLTISKEMSPBPENIDGNDLFFQKRVPGHDDKIQFESSLY 157
 Db 38 FGRLHCTAVIRNINDQVLFVKRQPVEDMDTIDQSASEPOTRLIYMKOSEVRGLA 97

QY 120 GHFLACOKEDDAFKLILKKDENGDKSYMTLNUQS 153
 Db 158 GFYFLACOKEDDAFKLILKKDENGDKSYMTLNUQS 191

Query Match Best Local Similarity 89.9%; Pred. No. 1.6e-60; Matches 142; Conservative 10; Mismatches 5; Indels 1; Gaps 1;

RESULT 4
 IL18_HUMAN STANDARD; PRT: 193 AA.

RESULT 5

| | | | |
|------------|--|-------------------------------|---------|
| IL1B_CANFA | STANDARD; | PRT; | 193 AA. |
| ID | IL1B_CANFA | | |
| AC | Q9XSO0; | | |
| DT | 30-MAY-2000 (Rel. 39, last sequence update) | | |
| DE | (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA). | | |
| GN | IL1B OR IGIF | | |
| OS | Homo sapiens (Human). | | |
| OC | Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | |
| RN | [1] | | |
| RR | SEQUENCE FROM N.A. | | |
| RC | TISSUE=LIVER; | | |
| RK | MEDLINE; 95247-646. | | |
| RA | Ushio S., Namba M., Okura T., Hattori K., Nakada Y., Akita K., Toriose K., Tanimoto T., | | |
| RA | Tanabe F., Konishi K., Micaleff M., Fujii M., Toriose K., Tanimoto T., | | |
| RA | Fukuda S., Ikeda M., Okamura H., Kurimoto M., | | |
| RT | "Cloning of the cDNA for human IFN-gamma-inducing factor, expression in Escherichia coli, and studies on the biologic activities of the protein." | | |
| RT | J. Immunol. 156:4274-4279(1996). | | |
| RN | [2] | | |
| RP | SEQUENCE FROM N.A. | | |
| RA | Yong D., Guixin D., Libua H., Haitao W.; | | |
| RT | "Cloning and sequencing of the cDNA for precursor IL-18." | | |
| RL | Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases. | | |
| RN | [3] | | |
| RP | SEQUENCE OF 2-193 FROM N.A. | | |
| RC | TISSUE=PERIPHERAL BLOOD; | | |
| RA | Conti B., Kim S.-J., Tinti C., Chun H.S., Joh T.H., | | |
| RL | Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases. | | |
| CC | -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I CELLS. | | |
| CC | -!- SUBCELLULAR LOCATION: SECRETED. | | |
| CC | -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY. | | |
| CC | -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY. | | |
| CC | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation in the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). | | |
| CC | DR | KW CYtokine. | |
| CC | DR | FT PROPEP 1 36 BY SIMILARITY. | |
| CC | FT CHAIN 37 193 AA; 22037 MW; 0973E586F461F25 CRC64; | | |
| CC | FT SEQUENCE 193 AA; 22037 MW; 0973E586F461F25 CRC64; | | |
| CC | DR | EMBL: Y11133; CBA72015.1. | |
| CC | DR | KW CYtokine. | |
| CC | DR | FT PROPEP 1 36 BY SIMILARITY. | |
| CC | FT CHAIN 37 193 AA; 22037 MW; 0973E586F461F25 CRC64; | | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; -. | |
| CC | DR | EMBL: M00553; -. | |
| CC | DR | EMBL: D45950; BA08106.1; -. | |
| CC | DR | EMBL: A507761; AAC27871; -. | |
| CC | DR | EMBL: U90434; BAB50010.1; - | |

RA Foss D.L., Murtaugh M.P.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DDJB databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Muneta T., Moi Y.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DDJB databases.
 CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
 CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
 CC CELLS (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC DR EMBL; 068701; AAC18415.1; -.
 CC DR EMBL; AB010003; BAA24135.1; -.
 CC KW CYTOKINE.
 CC FT PROPEP 1 35 BY SIMILARITY.
 CC SQ SEQUENCE 192 AA; 22026 MW; 881EA654E221A17A CRC64;
 CC
 CC Query Match 63.0%; Score 509; DB 1; Length 192;
 CC Best Local Similarity 64.9%; Pred. No. 9.1e-40;
 CC Matches 100; Conservative 26; Mismatches 26; Indels 2; Gaps 2;
 CC
 CC QY 2 FGRLHCTTAVIRNINDQVLIFVDR-KQPVFEDMDIDOSASEPOTRLIYMYKQSEVRGLA 60
 CC Db 37 FGKLEPKLKSITRNLDNQVLFINQHQAVFEDMPDPSDCSDNAPQTVFLLYMKDSLTRGLA 96
 CC
 CC QY 61 VTLVKDKSKTSLCKNKISIYEENDPPNNIDQIQSDLIFFKRVPGH-NKMFESSIVE 119
 CC Db 97 VTLVYQCKKHMSTLCKNKISIYEENDPPNNIDQIQSDLIFFKRVPGH-NKMFESSIVE 119
 CC
 CC QY 120 GHFLACQKEDDAFKLKKDENGDKSYMFTLW 153
 CC Db 157 GHFLACKEDDAFKLKKDENGDKSYMFTLW 190
 CC
 CC RESULT 7
 CC ID LON_HAEIN STANDARD; PRT; 803 AA.
 CC AC P43694;
 CC DT 01-NOV-1995 (Rel. 32, Created)
 CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
 CC DT 01-OCT-1996 (Rel. 34, Last annotation update)
 CC DE ATP-DEPENDENT PROTEASE LA (EC 3.4.21.53).
 CC LON OR LON-A OR H10462.
 CC OS Haemophilus influenzae.
 CC OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 CC OC Haemophilus.
 CC [1]
 CC SEQUENCE FROM N.A.
 CC RP STRAIN=RD / KW20;
 CC RC MEDLINE; 95356630.
 CC RX
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKinney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shriray R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cottrell M.D.,
 RA Utterback T.R., Hama M.C., Nguyen D.T., Sauder D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
 RA Gneh C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "whole-genome random sequencing and assembly of Haemophilus
 RT influenzae Rd", Science 269:95-112(1995).
 RT
 CC -!- FUNCTION: DEGRADES SHORT-LIVED REGULATOR AND ABNORMAL PROTEINS
 CC IN PRESENCE OF ATP. DEGRADES THE REGULATORY PROTEINS RCSA AND
 CC SULA. HYDROLYSES TWO AMPS FOR EACH PEPTIDE BOND CLEAVED IN THE
 CC PROTEIN SUBSTRAT (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF LARGE PROTEINS SUCH AS GLOBIN,
 CC CASEIN AND DENATURATED SERUM ALBUMIN. IN PRESENCE OF ATP,
 CC -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO CYTODERMAL FAMILY S16; ALSO KNOWN AS THE
 CC LON FAMILY OF ATP-DEPENDENT PROTEASES.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC DR EMBL; 032729; AAC22121.1; -.
 CC DR ITGR; H10462; -.
 CC DR INTERPRO; IPR001939; -.
 CC DR INTERPRO; IPR001984; -.
 CC DR PFAM; PF00004; AAA; 1.
 CC DR PRINTS; PRO0830; ENDOL-APTASE.
 CC DR PROSITE; PS01046; LON_SER; 1.
 CC FT KW Hydrolase; Serine protease; ATP-binding.
 CC FT NP_BIND 356 363 BY SIMILARITY.
 CC FT ACT_SITE 679 679 ATP (POTENTIAL).
 CC SQ SEQUENCE 803 AA; 89347 MW; 9E590852611EEA5B CRC64;
 CC
 CC Query Match 10.2%; Score 82.5; DB 1; Length 803;
 CC Best Local Similarity 18.9%; Pred. No. 4.3;
 CC Matches 44; Conservative 33; Mismatches 71; Indels 85; Gaps 7;
 CC
 CC QY 3 GRILHCTTAVIRNIND-QVLVFDKR---OPVFEDMDIDQAS--- 40
 CC Db 30 GRAKSINALEEAMDDKQILLYQSRAEADLEPTPEDLFQGTTIANIIQLIKLPDTVKVL 89
 CC
 CC QY 41 -EPOTRLIYMYKDSE-----VRLGAVTLVSKDSKXSTSCKNLISEE 83
 CC Db 90 VRGQRNRAKINSLEDGEQFSQAITPIETTYGDEKELVAVKSAVUSEEFVNLTNLNVKPTD 149
 CC
 CC QY 84 EMPPPEHIDI----- 103
 CC Db 150 LINALQIIDDYVRLADMMAHLPLVSPVSRHKQNQALEANQVERLEYLLGMMEADELTQVEK 209
 CC
 CC QY 104 RYPGHNMEFESSLYSLYQHFLACQKEDDAFKLKKDENGDKSYMFTLW 156
 CC Db 210 RIRGRVVKQMEKS-ORNYYL---NEQIKAIRKEMGGENDTIDEVEQLHQ 256
 CC
 CC RESULT 8
 CC ID IL1B_PIG STANDARD; PRT; 267 AA.
 CC AC P26889;
 CC DT 01-AUG-1992 (Rel. 23, Created)
 CC DT 30-MAY-2000 (Rel. 39, Last annotation update)
 CC DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
 CC GN IL1B.
 CC OS Sus scrofa (Pig).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE; 93314975.
 CC RA Huetter M.J., Lin G., Smith D.M., Murtaugh M.P., Molitor T.W.;
 CC RT "Cloning, sequencing and regulation of an mRNA encoding porcine
 CC interleukin-1 beta";
 CC RT Gene 129:285-289(1993).
 CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES. IL-1 STIMULATES

CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE; B-CELL
 CC MATURATION & PROLIFERATION; & FIBROBLAST GROWTH FACTOR ACTIVITY.
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
 CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
 CC -!- SUBUNIT: MONOMER.
 CC DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
 CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
 CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
 CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
 CC OR IS SECRETED BY A MECHANISM DIFFERENT FROM THAT USED FOR OTHER
 CC SECRETORY PROTEINS.
 CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC CCGF; P01584; IHB;
 DR HSSP; P01584; IHB;
 DR INTERPRO; IPR000975; -
 DR PFAM; PF002340; -
 DR PRINTS; PR00262; IILHBF
 DR PROSITE; PS00233; INTERLEUKIN_1
 KW CYTOKINE; Macrophage; Mitogen; Inflammatory response; Pyrogen.
 FT PROPEP 1 114 267 INTERLEUKIN_1 BETA.
 FT CHAIN 115 267 INTERLEUKIN_1 BETA.
 SQ SEQUENCE 267 AA; 30404 MW; 7F6B92B784D5086F CRC64;

Query Match 10.1%; Score 82; DB 1; Length 267;
 Best Local Similarity 26.1%; Pred. No. 1.3; Matches 23; Indels 31; Gaps 5;
 Matches 23; Conservative 22; Mismatches 31; Indels 12; Gaps 5;

Qy 49 YMKVDPSEVRGLAVLVLPSKDKSKTLCKNN---LISEEMPP--PENIDIOSSLIFF 101
 Db 160 FVGGDDPSNNKKPVPYIGK-GKNNLSCVMNDTPQLQEDIPKRYPKR--DMKRFVFF 216

Qy 102 QKRYPGHNSKMEPFESSLYEFGHFLACQKED 129
 Db 217 KTEI--KNRVEFESALYPNWYISTSOAE 242

RESULT 9

2ABA_YEAST STANDARD; PRT; 526 AA.

Qy 14 NINDOVL-FVDRQPPFEDMDIDIOSASEPQRLLIYMYKUDSEVRGLAVLTVSKDKXST 72
 Db 213 DIPPOGSFNIVDIKPTNMEELTEVITSAAFHPOECNLFFMISSK---GTIKCDMRS 267

Qy 73 LSCKRKIKLISFEEDPMDIDIOSLFLQKRYPGHNSKMEPFESSLYEFGHFLACQKEDAF 132
 Db 268 L-CDKNTKTFEYFLDINHN-----FFETTSISDIKFSNP--GRYIASRD---- 311

Qy 133 KLIKKKUENGOKSVMTLNHQ 156
 Db 312 YLTIVKWIWDVNMDNKPLKTI-NIHE 334

RESULT 10

IL1B_BOVIN STANDARD; PRT; 266 AA.

RP SEQUENCE FROM N_A.
 RC STRAIN-S88C / F11679;
 RX MEDLINE: 9719/971;
 RA Coglevina M., Klima R., Bertani I., Delneri D., Zaccaria P.,
 RA Bruschi C.V.;
 RT "Sequencing of a 40.5 kb fragment located on the left arm of
 RT chromosome VII from *Saccharomyces cerevisiae*.";
 RL Yeast 13:55-64(1997).
 CC -!- FUNCTION: PHOSPHATASE 2A AFFECTS A VARIETY OF BIOLOGICAL PROCESSES
 CC IN THE CELL SUCH AS TRANSCRIPTION, CELL CYCLE PROGRESSION AND
 CC CELULAR MORPHOGENESIS, AND PROVIDES AN INITIAL IDENTIFICATION OF
 CC CRITICAL SUBSTRATES FOR THIS PHOSPHATE. THE REGULATORY SUBUNIT
 CC MAY DIRECT THE CATALYTIC SUBUNIT TO DISTINCT, ALBEIT OVERLAPPING,
 CC SUBSETS OF SUBSTRATES.
 CC -!- SUBUNIT: PP2A EXISTS IN SEVERAL TRIMERIC FORMS, ALL OF WHICH
 CC CONSIST OF A CORE COMPOSED OF A CATALYTIC SUBUNIT ASSOCIATED WITH
 CC A 65 kDa (PR55) (SUBUNIT A) AND A 55 kDa (PR55) (SUBUNIT B)
 DR REGULATORY SUBUNIT. BY SIMILARITY.
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
 CC FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL: M72716; AA03442.1; -
 DR EMBL; X91837; CA62944.1; -
 DR EMBL; X91489; CA62785.1; -
 DR PIR; A41698; A41698.
 DR SGD; S0003158; CDB2.
 DR INTERPRO; IPR000099; -
 DR PRAM; PF01240; PR55_1; -
 DR PRAM; PR00000; PP2APR55.
 DR PROSITE; PS01024; PR55_1.
 DR PROSITE; PS01025; PR55_2; 1.
 DR KW CELL CYCLE.
 DR DOMAIN 416 419 POLY-SER.
 DR CONFLICT 500 500 T->N (IN REF. 1).
 SQ SEQUENCE 526 AA; 59662 MW; 60A12280FFA6782 CRC64;

Query Match 9.8%; Score 79.5; DB 1; Length 526;
 Best Local Similarity 25.8%; Pred. No. 4.9; Matches 36; Indels 23; Gaps 7;
 Matches 36; Conservative 29; Mismatches 56; Indels 23; Gaps 7;

Qy 14 NINDOVL-FVDRQPPFEDMDIDIOSASEPQRLLIYMYKUDSEVRGLAVLTVSKDKXST 72
 Db 213 DIPPOGSFNIVDIKPTNMEELTEVITSAAFHPOECNLFFMISSK---GTIKCDMRS 267

Qy 73 LSCKRKIKLISFEEDPMDIDIOSLFLQKRYPGHNSKMEPFESSLYEFGHFLACQKEDAF 132
 Db 268 L-CDKNTKTFEYFLDINHN-----FFETTSISDIKFSNP--GRYIASRD---- 311

Qy 133 KLIKKKUENGOKSVMTLNHQ 156
 Db 312 YLTIVKWIWDVNMDNKPLKTI-NIHE 334

RESULT 11

IL1B_BOVIN STANDARD; PRT; 266 AA.

RX MEDLINE: 9201758.
 RA Healy A.M., Zolnierowicz S., Stapleton A.E., Goebel M.,
 RA Deacon-Roach A., Pringle J.R.;
 RT "Cdc55, a *Saccharomyces cerevisiae* gene involved in cellular
 morphogenesis: identification, characterization, and homology to the
 RT B subunit of mammalian type 2A protein phosphatase.",
 RL Mol. Cell. Biol. 11:5767-5780(1991).
 RN [2]

Page 6

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovine; Bos.
 RN [1] SEQUENCE FROM N.A.
 RX MEDLINE: 8901591.
 RA Leong S.R., Flagg G.M., Lawman M., Gray P.W.;
 RT "The nucleotide sequence for the cDNA of bovine interleukin-1 beta."
 RL Nucleic Acids Res. 16:9054-9054(1988).
 RN [2] SEQUENCE FROM N.A.
 RP MEDLINE: 88310652.
 RX Maliszewski C.R., Baker P.E., Schoenborn M.A., Davis B.S., Cosman D.,
 RA Gillis S., Cerretti D.P.;
 RT "Cloning, sequence and expression of bovine interleukin 1 alpha and
 interleukin 1 beta complementary DNAs."
 RL Mol. Immunol. 25:425-437(1988).
 CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
 THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
 NATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
 IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
 THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
 CC -!- SUBUNIT: MONOMER.
 CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
 AMINO ACIDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
 CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
 PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
 OR IS SECRETED BY A MECHANISM DIFFERENT FROM THAT USED FOR OTHER
 SECRETORY PROTEINS.
 CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M3589; AA30585.1; -.
 DR EMBL; X12498; CAA3018.1; -.
 DR EMBL; M07211; AAA30584.1; -.
 DR PIR; JL0010; ICB01B.
 DR HSSP; P01584; 1HB.
 DR INTERPRO; IPR000975; -.
 DR PFAM; PF00340; interleukin-1.
 DR PRINS; PR00262; ILIHBGF.
 DR PROSITE; PS00253; INTERLEUKIN1.
 DR CYCLOM; Macrophage; Mitogen; Inflammatory response; Pyrogen.
 FT PROPEP 1 113
 FT CHAIN 114 266
 FT CONFLICT 252 252
 SQ SEQUENCE 266 AA; 30774 MW; 9D1EF8F575070586 CRC64;

 Query Match 9.7%; Score 78; DB 1; Length 1196;
 Best Local Similarity 24.3%; Pred. No. 18;
 Matches 35; Conservative 23; Mismatches 58; Indels 28; Gaps 8;
 QY 35 IDQASSEPQTALIYMKDVERGLAV--TLSVKOSKXSTLSCKNNKISIEMDPEN-- 90
 Db 965 ISISVRLKDQLLIFT-NDKVNAYNSIDQINISYNTNISLWNKNNSIVYELSVLDNP1 10
 QY 91 -----IDQISDLIPKQKRVPGHNMKEFFSSLVMEGHFLAQKEDDAFK 13
 Db 1024 TSEEVRNFSYLDNSYIROSSSLNEYNKQYQLYWVFPTSLV-----VNDDNSY 10
 QY 134 LITKKIDENGDKSVMTLNHS 157
 Db 1078 LSLKNIDGINISSVRFKLINIDES 1101

 RESULT 12
 U3A_MOUSE
 ID U3A_MOUSE STANDARD; PRT; 885 AA.
 AC 008759; P91482;
 AC 008759; P91482;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE UBIQUITIN-PROTEIN LIGASE E3A (EC 6.3.3.2-) (ONCOGENIC PROTEIN-
 DE ASSOCIATED PROTEIN EG-AP).
 GN UBE3A.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1] SEQUENCE FROM N.A.
 RP

OC Helicobacter.
 RN SEQUENCE FROM N A.
 RP STRAIN=26695 / ATCC 700392;
 RA MEDLINE: 97394467.
 RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
 Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
 Nelson K., Quackenbush J.J., Zhou L., Kirkness E.F., Peterson S.,
 Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
 McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
 Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
 Cottrell M.D., Weidman J.M., Fujii C., Bowman C., Wathey L., Wallin E.,
 Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
 Venter J.C.;
 RT "The complete genome sequence of the gastric pathogen Helicobacter
 pylori";
 RL Nature 388:539-547(1997).
 CC -1- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY
 CC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AE00541; AAD07278.1; -.
 DR HSSP; P07900; 1YES.
 DR IPR01404; -.
 DR PFAM; PF00183; HSP90; 1.
 DR PROSITE; PRO0775; HEATSHOCK90.
 DR PS0298; HSP90; 1.
 KW Chaperone; ATP-binding; Heat shock
 SEQUENCE 621 AA; 71274 MW; 28F19C1DCTEAD9A CRC64;
 SQ

Query Match 9.5%; Score 76.5; DB 1; Length 706;
 Best Local Similarity 22.2%; Pred. No. 13;
 Matches 35; Conservative 25; Mismatches 63; Indels 35; Gaps 6;
 Matches 35; Conservative 25; Mismatches 63; Indels 35; Gaps 6;

QY 9 TAVERNINDQFLVFDKRDQPVFEDMTDIDQASBPQT---RLLIYMDKSEVRGLAVTLS 64
 Db 428 TSTVQNSNTNL---SROPILVQGDVDEDAPSEST-NGTPFLFYKEQSNVE---YS 478
 QY 65 VKDSXXLSCKNKKISFE--EMDPPEMIDIQSDFLFFQKRVPGH----- 108
 Db 479 NNESMGSQMPFRKLPTTEALQLOQHKRNITDARE-IDNSKSNDSHVLPGNGTRYSDA 537
 QY 109 ----NKMFESSLYEGIRFLACOKEDDAFKLILKKDE 141
 Db 538 DYKETEPPIEFKYPGEGPCRAGGLEVKRMFSKKNE 575

Query Match 9.5%; Score 76.5; DB 1; Length 621;
 Best Local Similarity 23.2%; Pred. No. 11;
 Matches 29; Conservative 27; Mismatches 52; Indels 17; Gaps 4;

QY 32 MTDIDOSASEPOTRLIYMDKSEVRGLAVTLSVK---DKXSTLSCKNKKISFEDEMPP 88
 Db 31 LRELVLNSASDALDKLNLYMLTDDEKLKGQNTTPSILSFSDFDSQKTLTKIGMDKNDLI 90

QY 89 EIMDDI-QSDLIFFQKRPVGHNKM-----EEFSSLYEGIFLACOKEDDAFKLILKKDE 141
 Db 91 EHGTIAKSGTKNFSALSGDKKKDSALIG3FGVGFYSANHVAS-----KIVQVTKKV 143

QY 142 NGDKS 146
 QY 144 NSDQA 148

RESULT 15
 YK10_YEAST STANDARD PRT; 706 AA.
 AC P36166;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE HYPOTHETICAL 79.4 KDA PROTEIN IN PRP16-SRP40 INTERGENIC REGION.
 GN YER090W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC [1]
 OC Saccharomycetidae; Saccharomyces.
 OC SEQUENCE FROM N A.
 RA Baladron V., Ballesta J.P.G., Bou G., del Rey F., Esteban P.F., Garcia-Cantalejo J.M., Garcia-Ramirez J.J., Gonzalez A., Jimenez A.,
 RA